Ness-ender (

# RAW SEQUENCE LISTING ERROR REPORT



#9

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/224, 15/
Art Unit / Team No.: 16/8

Date Processed by STIC:

THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.

PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,
- 2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY

THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.

IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:

ARTI SHAH 703-308-4212

#### Raw Sequence Listing Error Summary

| )          | ERROR DETECTED                   | SUGGESTED CORREC  | CTION                           | SERIAL NUMBER: 09/229757                          |
|------------|----------------------------------|---|---------------------------------|---|
| ATT        | N: NEW RULES CASES:              | PLEASE DISREGARD ENGLI                                  | SH "ALPHA" HEADERS, \           | WHICH WERE INSERTED BY PTO SOFTWARE               |
| 1 0        | Wrapped Nudelcs                  | The number/text at the end                              |                                 |   |
|            |                                  | This may occur if your file w                           | as retrieved in a word proce    | ssor after creating it.                           |
|            |                                  | Please adjust your right ma                             | rgin to .3, as this will preven | it "wrapping".                                    |
| 2          | Wrapped Aminos                   | The amino acid number/text                              | at the end of each line wra     | pped * down to the next line.                     |
|            | -                                | This may occur if your file w                           | as retrieved in a word proce    | essor after creating it.                          |
|            |                                  | Please adjust your right man                            | gin to .3, as this will preven  | t "wrapping".                                     |
| 3          | Incorrect Line Length            | The rules require that a line i                         | not exceed 72 characters in     | length. This includes spaces.                     |
|            |                                  | All text must be visible on pa                          | age.                            |   |
| 4          | _ Misaligned Amino Add           |   |                                 | . This may be caused by the use of labs           |
| •          | Numbering                        | between the numbering. It is                            | recommended to delete an        | y tabs and uses spacing between the numbers.      |
| 5          | _ Non-ASCII                      | This file was not saved in AS                           | CII (DOS) lext, as required     | by the Sequence Rules.                            |
|            |                                  | Please ensure your subsequ                              | ent submission is saved in a    | ASCII text so that it can be processed.           |
| 6          | _ Variable Length                | Sequence(s) contain n'                                  | s or Xaa's which represente     | d more than one residue.                          |
|            | •                                | As per the rules, each n or X                           |                                 |   |
|            |                                  | Please present the maximum                              |                                 |   |
|            | : <b>ķ</b>                       | Indicate in the (ix) features s                         | ection that some may be mi      | ssing.  |
| 7          | _ Wrong Designation              |   |                                 | signators which are not standard                  |
| 1          |                                  | representations as per the Se $1837-38$ ,               | 46-50,57-59                     | 7/-79 88-98,709                                   |
| 8 <u>J</u> | Skipped Sequences                | • • • • • • •   |                                 | following format for each skipped sequence:       |
|            | (OLD RULES)                      | (2) INFORMATION FOR SEC                                 |                                 | headings under "SEQUENCE CHARACTERISTICS")        |
|            |                                  | (xI) SEQUENCE DESCRIPTI                                 |                                 |   |
|            |                                  | This sequence is intentiona                             |                                 |   |
|            |                                  | Please also adjust the *(iii) NU                        | IMBER OF SEQUENCES:             | response to include the skipped sequence(s).      |
| _          |                                  | ,   |                                 |   |
| 9          | Skipped Sequences (NEW RULES)    |   | intentional, please use the     | following format for each skipped sequence.       |
|            | (NEW MOCES)                      | <210> sequence id number <400> sequence id number       |                                 | •   |
|            |                                  | 000   |                                 |   |
| 10         | Use of n's or Xaa's              | Use of n's and/or Xaa's have t                          | een detected in the Seque       | nce Usting.                                       |
|            | (NEW RULES)                      | Use of <220> to <223> is MAI                            |                                 |   |
|            |                                  | In <220> to <223> section, ple                          | ase explain location of n or    | Xaa, and which residue n or Xaa represents.       |
| 11         | Use of <213>Organism (NEW RULES) | Sequence(s) are mis                                     | sing this mandatory field or    | its response.                                     |
| 12         | Use of <220>Feature              | Saguagada) ara missiag                                  | the <220>Feeburg and acc        | ociated headings                                  |
|            |                                  | Sequence(s) are missing<br>Use of <220> to <223> is MAN |                                 | SM is "Artificial" or "Unknown"                   |
|            |                                  | Please explain source of ger                            |                                 |   |
|            |                                  | (See "Federal Register,"                                | 6/01/98, Vol. 63, No. 1         | 04, pp. 29631-32)                                 |
| ,          |                                  | (Sec. 1.823 of new Sequ                                 | ence Rules)                     |   |
| 13         |                                  |   |                                 | version 2.0. This causes a corrupted              |
|            |                                  | file, resulting in missing manda                        | tory numeric identifiers and    | responses (as Indicated on raw sequence listing). |
|            |                                  | nstead, please use "File Mana                           | per or any other means to       | copy file to floppy disk.                         |

## **SEQUENCE VERIFICATION REPORT** PATENT APPLICATION *US/09/229,751*

DATE: 04/27/1999 TIME: 10:35:34

| Line | Error   | Original Text                             |
|------|---|---|
| 28   | Wrong application Serial Number               | (A) APPLICATION NUMBER: US PCT/US99/00771 |
| 66   | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 87   | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 108  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 129  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 150  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 171  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 192  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 213  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 234  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 255  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 276  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 297  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 318  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 399  | Sequence 18 missing                           | (2) INFORMATION FOR SEQ ID NO:19:         |
| 672  | Sequence 32 thru 38 missing                   | (2) INFORMATION FOR SEQ ID NO:39:         |
| 819  | Sequence 46 thru 50 missing                   | (2) INFORMATION FOR SEQ ID NO:51:         |
| 946  | Sequence 57 thru 59 missing                   | (2) INFORMATION FOR SEQ ID NO:60:         |
| 949  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 970  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 983  | Wrong Sequence Number                         | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:  |
| 991  | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1012 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1033 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1054 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1075 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1096 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1117 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1138 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1159 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1177 | Sequence 71 thru 79 missing                   | (2) INFORMATION FOR SEQ ID NO:80:         |
| 1345 | Sequence 88 thru 98 missing                   | (2) INFORMATION FOR SEQ ID NO:99:         |
| 1390 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1411 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1432 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1453 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1474 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1495 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1516 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1537 | Entered (21) and Calc. Seq. Length (0) differ | (A) LENGTH: 21 base pairs                 |
| 1555 | Sequence 109 missing                          | (2) INFORMATION FOR SEQ ID NO:110:        |



## RAW SEQUENCE LISTING PATENT APPLICATION US/09/229,751

DATE: 04/27/1999 TIME: 10:35:28

INPUT SET: S31624.raw

This Raw Listing contains the General Information Section and those Sequences containing ERRORS.

Does Not Comply
Corrected Diskette Needed

|   | 1        | SEQUENCE LISTING  |
|---|----------|---|
|   | 2        |   |
|   | 3        | (1) General Information:  |
|   | 4        |   |
|   | 5        | (i) APPLICANT: Turnbough Jr., Charles L   |
|   | 6<br>7   | (ii) MIMIN ON THURWITON D. III I I  |
|   | 8        | (ii) TITLE OF INVENTION: Peptide Ligands That Bind to Surfaces  |
|   | 9        | ·- · · · · · · · · · · · · · · · · · ·  |
|   |          | Bacterial Spores  |
|   | 10<br>11 | (iii) NUMBER OF GROUPHORG (OD ) / / O O O Standy  |
|   | 12       | (111) NOMBER OF SEQUENCES: (80)/// //DC // // // // //////////////////  |
|   | 13       | (iii) NUMBER OF SEQUENCES: (80)/// (see item 8 or Even Summing (iv) CORRESPONDENCE ADDRESS:   |
|   | 14       | (A) ADDRESSEE: Hendricks and Associates   |
|   | 15       | (A) ADDRESSEE: Hendricks and Associates (B) STREET: P.O. Box 2509   |
|   | 16       | (C) CITY: Fairfax   |
|   | 17       | (C) CIII: FAIIIAX (D) STATE: VA   |
|   | 18       | (E) COUNTRY: USA  |
|   | 19       | (E) COUNTRY: USA<br>(F) ZIP: 22031  |
|   | 20       | (F) EIF. 22031  |
|   | 21       | (V) COMPUTER READABLE FORM:   |
|   | 22       | (A) MEDIUM TYPE: Floppy disk  |
|   | 23       | (B) COMPUTER: IBM PC compatible   |
|   | 24       | (C) OPERATING SYSTEM: PC-DOS/MS-DOS   |
|   | 25       | (D) SOFTWARE: PatentIn Release #1.0, Version #1.25  |
|   | 26       |   |
|   | 27       | (vi) CURRENT APPLICATION DATA:  (A) APPLICATION NUMBER: US PCT/US99/00771  (B) FILING DATE: (14-JAN-1999)   |
| > | 28       | (A) APPLICATION NUMBER: US PCT/US99/00771   |
|   | 29       | (B) FILING DATE: (14-JAN-1999   |
|   | 30       | (VIII) ATTORNEY/AGENT INFORMATION:  (A) NAME: Hendricks, Glenna M  (B) FILING DATE: (14-JAN-1999  (VIII) PRIOR APPLICATION PATA  (A) APPLICATION PATA |
|   | 31       | Wish Ming APPI I CATION PATA  |
|   | 32       | (Viii) ATTORNEY/AGENT INFORMATION:  |
|   | 33       | (A) NAME: Hendricks, Glenna M (A) APPLICATION MUNISAR:  |
|   | 34       | (B) REGISTRATION NUMBER: 32,535 (C) REFERENCE/DOCKET NUMBER: turnbough (B) FILING DATE:   |
|   | 35       | (C) REFERENCE/DOCKET NUMBER: turnbough (B) P/L/NV VIII  |
|   | 36       |   |
|   | 37       | (ix) TELECOMMUNICATION INFORMATION:   |
|   | 38       | (A) TELEPHONE: (703) 591-4470   |
|   | 39       | (B) TELEFAX: (703) 591-4428   |
|   | 40       |   |
|   | 41       |   |
|   |          | •   |

#### **ERRORED SEQUENCES FOLLOW:**

## RAW SEQUENCE LISTING PATENT APPLICATION US/09/229,751

DATE: 04/27/1999 TIME: 10:35:28

|   |     |  | HALOI PET. PRIORA                              |
|---|-----|--|--|
|   | 63  | (2) INFORMATION FOR SEQ ID NO:2:                         |  |
|   | 64  |  |  |
|   | 65  | (i) SEQUENCE CHARACTERISTICS:                            |  |
| > | 66  | (A) LENGTH: 21 base pairs                                |  |
|   | 67  | (B) TYPE: nucleic acid                                   |  |
|   | 68  | (C) STRANDEDNESS: single                                 | a lave   |
|   | 69  | (D) TOPOLOGY: linear                                     | Of St.   |
|   | 70  |  | N =  |
|   | 71  | (ii) MOLECULE TYPE: DNA (genomic)                        | Sometern<br>se ten I on<br>Ever Sunnay Meet    |
|   | 72  |  | John -   |
|   | 73  | (iii) HYPOTHETICAL: NO                                   | 1  |
|   | 74  |  | 101 ten I                                      |
|   | 75  | (iv) ANTI-SENSE: NO                                      | 120 2  |
|   | 76  | ·  | C Lumen Mel                                    |
|   | 77  |  | >MM AUTHOR                                     |
|   | 78  |  |  |
| • | 79  | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:                  | <b>~</b> i                                     |
|   | 80  |  | 201  |
|   | 81  | AATCATTTT TGATTAAGCC G                                   |  |
|   | 82  | 21   |  |
|   | 83  |  |  |
|   | 84  | (2) INFORMATION FOR SEQ ID NO:3:                         |  |
|   | 85  | (2) 2.02 01  |  |
|   | 86  | (i) SEQUENCE CHARACTERISTICS:                            |  |
| > | 87  | (A) LENGTH: 21 base pairs                                |  |
|   | 88  | (B) TYPE: nucleic acid                                   |  |
|   | 89  | (C) STRANDEDNESS: single                                 | 1 MM   |
|   | 90  | (D) TOPOLOGY: linear                                     | 15001.   |
|   | 91  | (2) 200 220 2  | same   |
|   | 92  | (ii) MOLECULE TYPE: DNA (genomic)                        | 011  |
|   | 93  | (/   | <i>y</i> • • • • • • • • • • • • • • • • • • • |
|   | 94  | (iii) HYPOTHETICAL: NO                                   |  |
|   | 95  | <b>( ' /</b>   |  |
|   | 96  | (iv) ANTI-SENSE: NO                                      |  |
|   | 97  | ( /  |  |
|   | 98  | •  |  |
|   | 99  |  |  |
|   | 100 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:                  |  |
|   | 101 | ·  |  |
|   | 102 | AATCATTTTT TGAGGTCTCC G                                  |  |
|   | 103 | 21   |  |
|   | 104 |  |  |
|   |     | 10) THEORY MICH COD CEO ID NO.4.                         |  |
|   | 105 | (2) INFORMATION FOR SEQ ID NO:4:                         |  |
|   | 106 | (i) SEQUENCE CHARACTERISTICS:                            |  |
|   | 107 | (1) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs |  |
| > | 108 | (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid         |  |
|   | 109 |  |  |
|   | 110 | (C) STRANDEDNESS: single                                 |  |
|   | 111 | (D) TOPOLOGY: linear                                     |  |
|   | 112 | () A MOTHER TOPE, DNA (conomic)                          |  |
|   | 113 | (ii) MOLECULE TYPE: DNA (genomic)                        |  |
|   |     |  |  |

### RAW SEQUENCE LISTING PATENT APPLICATION US/09/229,751

DATE: 04/27/1999 TIME: 10:35:29

```
114
        (iii) HYPOTHETICAL: NO
115
116
117
         (iv) ANTI-SENSE: NO
118
119
120
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
121
122
123
     AATCATTTTC TGCCTCGTTG G
124
          21
125
      (2) INFORMATION FOR SEQ ID NO:5:
126
127
           (i) SEQUENCE CHARACTERISTICS:
128
129
                (A) LENGTH: 21 base pairs
                (B) TYPE: nucleic acid
130
131
                (C) STRANDEDNESS: single
132
                (D) TOPOLOGY: linear
133
          (ii) MOLECULE TYPE: DNA (genomic)
134
135
136
         (iii) HYPOTHETICAL: NO
137
         (iv) ANTI-SENSE: NO
138
139
140
141
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
142
143
144
      AATCATTTC TTCCTAAGGT G
145
          21
146
147
      (2) INFORMATION FOR SEQ ID NO:6:
148
149
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 21 base pairs
150
151
                (B) TYPE: nucleic acid
152
                (C) STRANDEDNESS: single
153
                (D) TOPOLOGY: linear
154
         (ii) MOLECULE TYPE: DNA (genomic)
155
156
         (iii) HYPOTHETICAL: NO
157
158
159
         (iv) ANTI-SENSE: NO
160
161
162
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:
163
164
```

## RAW SEQUENCE LISTING PATENT APPLICATION US/09/229,751

DATE: 04/27/1999 TIME: 10:35:29

|    |            |   | INPUT SET: S31624.raw |
|----|------------|---|-----------------------|
|    | 165        | AATCATTTTC TGTTGCCGCC G                                     | same                  |
|    | 166        | 21  | JW.                   |
|    | 167        |   |                       |
|    | 168        | (2) INFORMATION FOR SEQ ID NO:7:                            |                       |
|    | 169        | (2) INFORMATION FOR SEQ ID NO: /:                           |                       |
|    | 170        | (i) SEQUENCE CHARACTERISTICS:                               |                       |
|    |            | (A) LENGTH: 21 base pairs                                   |                       |
| -> | 171        |   |                       |
|    | 172        | (B) TYPE: nucleic acid                                      | ļ.                    |
|    | 173        | (C) STRANDEDNESS: single                                    |                       |
|    | 174        | (D) TOPOLOGY: linear  |                       |
|    | 175        | (11) MATERIAL MINE DIVINING                                 |                       |
|    | 176        | (ii) MOLECULE TYPE: DNA (genomic)                           |                       |
|    | 177        |   |                       |
|    | 178        | (iii) HYPOTHETICAL: NO                                      |                       |
|    | 179        |   | 1                     |
|    | 180        | (iv) ANTI-SENSE: NO   |                       |
|    | 181        |   |                       |
|    | 182.       |   |                       |
|    | 183        |   |                       |
|    | 184        | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:                     | 1                     |
|    | 185        | •   |                       |
|    | 186        | AATCATTTTT TGCCTCCTCG G                                     |                       |
|    | 187        | 21  |                       |
|    | 188        |   |                       |
|    |            | AAA TYPARYARTAY DAR GEO IR NO A                             |                       |
|    | 189        | (2) INFORMATION FOR SEQ ID NO:8:                            |                       |
|    | 190        |   |                       |
|    | 191        | (i) SEQUENCE CHARACTERISTICS:                               |                       |
| -> | 192        | (A) LENGTH: 21 base pairs                                   |                       |
|    | 193        | (B) TYPE: nucleic acid                                      |                       |
|    | 194        | (C) STRANDEDNESS: single                                    |                       |
|    | 195        | (D) TOPOLOGY: linear  |                       |
|    | 196        |   |                       |
|    | 197        | (ii) MOLECULE TYPE: DNA (genomic)                           |                       |
|    | . 198      |   |                       |
|    | 199        | (iii) HYPOTHETICAL: NO                                      |                       |
|    | 200        |   | · ·                   |
|    | 201        | (iv) ANTI-SENSE: NO   |                       |
|    | 202        |   | 1                     |
|    | 203        |   | .1/                   |
| ,  | 204        |   | Ψ                     |
|    | 205        | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:                     | •                     |
|    | 206        |   |                       |
|    | 207        | AATCATTTTC TGCCTACTGG G                                     |                       |
|    | 208        | 21  |                       |
|    | 209        |   |                       |
|    | 210        | /2) THEODMARTON FOR CEO TO MO.C.                            |                       |
|    | 210<br>211 | (2) INFORMATION FOR SEQ ID NO:9:                            |                       |
|    |            | (i) GEOLIENGE GUADAGMEDICATOS.                              |                       |
|    | 212        | (i) SEQUENCE CHARACTERISTICS:                               |                       |
| -> | 213        | <pre>(A) LENGTH: 21 base pairs (B) TYPE: nucleic acid</pre> |                       |
|    | 214        |   |                       |

#### RAW SEQUENCE LISTING PATENT APPLICATION US/09/229,751

DATE: 04/27/1999 TIME: 10:35:29

```
(C) STRANDEDNESS: single
215
216
                (D) TOPOLOGY: linear
217
          (ii) MOLECULE TYPE: DNA (genomic)
218
219
         (iii) HYPOTHETICAL: NO
220
221
         (iv) ANTI-SENSE: NO
222
223
224
225
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
226
227
     AATCATTTTC TGATGCCGAA G
228
229
          21
230
231
     (2) INFORMATION FOR SEQ ID NO:10:
232
           (i) SEQUENCE CHARACTERISTICS:
233
                (A) LENGTH: 21 base pairs
234
235
                (B) TYPE: nucleic acid
236
                (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
237
238
          (ii) MOLECULE TYPE: DNA (genomic)
239
240
         (iii) HYPOTHETICAL: NO
241
242
243
         (iv) ANTI-SENSE: NO
244
245
246
247
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
248
     AATCATTTC TTAAGGGGAC G
249
250
          21
251
252
      (2) INFORMATION FOR SEQ ID NO:11:
253
254
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 21 base pairs
255
                (B) TYPE: nucleic acid
256
257
                (C) STRANDEDNESS: single
258
                (D) TOPOLOGY: linear
259
         (ii) MOLECULE TYPE: DNA (genomic)
260
261
         (iii) HYPOTHETICAL: NO
262
263
264
          (iv) ANTI-SENSE: NO
265
```

#### **RAW SEQUENCE LISTING** PATENT APPLICATION US/09/229,751

DATE: 04/27/1999 TIME: 10:35:30

```
266
267
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
268
                                                                   same
269
270
     ATTCATTTT TGCCGCAGAA T
271
         21
272
     (2) INFORMATION FOR SEQ ID NO:12:
273
274
           (i) SEQUENCE CHARACTERISTICS:
275
                (A) LENGTH: 21 base pairs
276
                (B) TYPE: nucleic acid
277
                (C) STRANDEDNESS: single
278
                (D) TOPOLOGY: linear
279
280
281
         (ii) MOLECULE TYPE: DNA (genomic)
282
         (iii) HYPOTHETICAL: NO
283
284
          (iv) ANTI-SENSE: NO
285
286
287
288
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
289
290
291
     ATTCATTTTC TTCTTTGGCG T
292
          21
293
      (2) INFORMATION FOR SEQ ID NO:13:
294
295
           (i) SEQUENCE CHARACTERISTICS:
296
                (A) LENGTH: 21 base pairs
297·
298
                (B) TYPE: nucleic acid
299
                (C) STRANDEDNESS: single
300 50
                (D) TOPOLOGY: linear
301
302
         (ii) MOLECULE TYPE: DNA (genomic)
303
         (iii) HYPOTHETICAL: NO
304
305
306
         (iv) ANTI-SENSE: NO
307
308
309
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:
310
311
     AATCATTTTC TGATTAGGAA G
312
313
          21
314
```

## RAW SEQUENCE LISTING PATENT APPLICATION US/09/229,751

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|    |            |  | INFUL SELL SS1024.74W                    |
|----|------------|--|--|
|    | 316        |  |  |
|    | 317        |  |  |
| >  | 318        | (A) LENGTH: 21 base pairs                    |  |
|    | 319        | (B) TYPE: nucleic acid                       |  |
|    | 320        | (C) STRANDEDNESS: single                     |  |
|    | 321        | (D) TOPOLOGY: linear                         |  |
|    | 322        |  | •  |
|    | 323        | <pre>(ii) MOLECULE TYPE: DNA (genomic)</pre> |  |
|    | 324        |  | 1 1 1 ml                                 |
|    | 325        | (iii) HYPOTHETICAL: NO                       |  |
|    | 326        | (i) NUMT CENTER, NO                          |  |
|    | 327        | (iv) ANTI-SENSE: NO                          | same                                     |
|    | 328<br>329 |  |  |
|    | 329        |  |  |
|    | 330        | (vi) SPONENCE DESCRIPTION, SPO ID NO.14      | •  |
|    | 331        | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14      | •  |
|    | 333        | AATCATTTTC TGCCGACTGC T                      |  |
|    | 334        | 21   |  |
|    | 335        | 1.   | 10 Mi Kack                               |
|    | 333        |  | & 18 mining my                           |
| >  | 399        | (2) INFORMATION FOR SEQ ID NO:19:            | z 18 minig (suback<br>pags)              |
|    | 400        | -  | Roya)                                    |
|    | 401        | (i) SEQUENCE CHARACTERISTICS:                | <i>  0 /</i>                             |
|    | 402        | (A) LENGTH: 7 amino acids                    | •  |
|    | 403        | (B) TYPE: amino acid                         |  |
|    | 404        | (C) STRANDEDNESS: single                     |  |
| 1  | 405        | (D) TOPOLOGY: linear                         | ·  |
|    | 406        |  |  |
| N/ | 407        | (ii) MOLECULE TYPE: peptide                  |  |
| 01 | 408        |  |  |
|    | 409        | (iii) HYPOTHETICAL: NO                       |  |
|    | 410        |  |  |
|    | 411        | (iv) ANTI-SENSE: NO                          |  |
|    | 412        |  |  |
|    | 413        |  |  |
|    | 414        |  |  |
|    | 415<br>416 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19      | •  |
|    | 415        | Asn His Phe Leu Ile Lys Pro                  |  |
|    | 417        | ASH HIS FRE LEG TIE BYS FIO                  | 1 00 1/ 120 0                            |
|    | 419        | 1 3  | 1 20 () Show 8 much                      |
|    |            |  | Jay 1/C3 C 34 8 1/10 Cong                |
| >  | 672        | (2) INFORMATION FOR SEQ ID NO:39:            | Sign 32 though 38 mining<br>(back pager) |
|    | 673        |  | ( fack room)                             |
|    | 674        | (i) SEQUENCE CHARACTERISTICS:                |  |
|    | 675        | (A) LENGTH: 5 amino acids                    |  |
|    | 676        | (B) TYPE: amino acid                         |  |
|    | 677        | (C) STRANDEDNESS: single                     |  |
|    | 678        | (D) TOPOLOGY: linear                         |  |
|    | 679        |  |  |
|    | 680        | (ii) MOLECULE TYPE: peptide                  |  |
|    | 681        |  | •  |
|    |            |  |  |

### RAW SEQUENCE LISTING PATENT APPLICATION US/09/229,751

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```
682
         (iii) HYPOTHETICAL: NO
683
684
          (iv) ANTI-SENSE: NO
685
686
687
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:
688
689
           Asn His Phe Leu Pro
690
                                                  Segr 46 Shroyt 50 mining
(hock pager)
691
692
      (2) INFORMATION FOR SEQ ID NO:51:
819
820
           (i) SEQUENCE CHARACTERISTICS:
821
                (A) LENGTH: 7 amino acids
822
                (B) TYPE: amino acid
823
                (C) STRANDEDNESS: single
824
                (D) TOPOLOGY: linear
825
826
          (ii) MOLECULE TYPE: peptide
827
828
829
         (iii) HYPOTHETICAL: NO
830
          (iv) ANTI-SENSE: NO
831
832
833
834
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:
835
836
           Lys Pro Arg Gln Pro Gly Leu
837
                                                   Jegn 51/ Shough 59 mining
838
839
946
      (2) INFORMATION FOR SEQ ID NO:60:
947
           (i) SEQUENCE CHARACTERISTICS:
948
                 (A) LENGTH: 21 base pairs
949
950
                 (B) TYPE: nucleic acid
951
                 (C) STRANDEDNESS: single
952
                 (D) TOPOLOGY: linear
953
954
          (ii) MOLECULE TYPE: DNA (genomic)
955
         (iii) HYPOTHETICAL: NO
956
957
958
          (iv) ANTI-SENSE: NO
959
960
961
962
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:
963
                        some frant eval as desployed en previous sequeros
      AATAGTGTTA CTCTTGAGCC G
964
```

## RAW SEQUENCE LISTING PATENT APPLICATION US/09/229,751

DATE: 04/27/1999 TIME: 10:35:31

|   |  |   | 114FU1 3E1; 331024.7UW |
|---|--|---|------------------------|
|   | 965  | 21  |                        |
|   | 966  |   |                        |
|   |  |   |                        |
|   | 967  | (2) INFORMATION FOR SEQ ID NO:61:   |                        |
|   | 968  |   |                        |
|   | 969  | (i) SEQUENCE CHARACTERISTICS:   |                        |
| > | 970  | (A) LENGTH: 21 base pairs   |                        |
|   | 971  | (B) TYPE: nucleic acid  |                        |
|   | 972  | (C) STRANDEDNESS: single  |                        |
|   | 973  | (D) TOPOLOGY: linear  |                        |
|   | 974  | (b) for obodi. Iffical  |                        |
|   | 975  | (ii) MOLECULE TYPE: DNA (genomic)   |                        |
|   |  | (II) MODECODE TIPE: DNA (Genomic)   |                        |
|   | 976  | (iii) uupomummaar. No   |                        |
|   | 977  | (iii) HYPOTHETICAL: NO  |                        |
|   | 978  | A' A SAME GENGE NO  |                        |
| • | 979  | (iv) ANTI-SENSE: NO   |                        |
|   | 980  | 1.1   |                        |
|   | 981  | . 91  |                        |
|   | 982  |   |                        |
| > | 983  | (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62/:  |                        |
|   | 984  |   | 4                      |
|   | 985  | AAGCCGAGGC AGCCGGGTTT G   | 1 2 0 0 000            |
|   | 986  | 21  | I mel sour             |
|   | 987  | •   |                        |
|   |  |   | Jornet end             |
|   | 988  | (2) INFORMATION FOR SEQ ID NO:62:   |                        |
|   | 989  |   |                        |
|   | 990  | (i) SEQUENCE CHARACTERISTICS:   |                        |
| > | 991  | (A) LENGTH: 21 base pairs   | •                      |
|   | 992  | (B) TYPE: nucleic acid  |                        |
|   | 993  | (C) STRANDEDNESS: single  |                        |
|   | 994  | (D) TOPOLOGY: linear  |                        |
|   | 995  |   |                        |
|   | 996  | (ii) MOLECULE TYPE: DNA (genomic)   |                        |
|   | 997  |   |                        |
|   | 998  | (iii) HYPOTHETICAL: NO  |                        |
|   | 999  | (/  |                        |
|   | 1000   | (iv) ANTI-SENSE: NO   |                        |
|   | 1001   | (4.7  |                        |
|   | 1002   |   |                        |
|   | 1002   |   |                        |
|   | 1003   | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:  |                        |
|   | 1004   | (NI) DEGORNOS DEDOKIFIION. DEG ID NO.02.  |                        |
|   | 1005   | TCTACTCCGG CGTGGCTGTC G   | 1                      |
|   |  | ICIACICOS COISSCISIC S  | 1 Lenan                |
|   |  | 21  |                        |
|   | 1007   | 21  | Sand Dod               |
|   |  | 21  | Jane 200               |
|   | 1007<br>1008                                 |   | fornet evol            |
|   | 1007<br>1008                                 | (2) INFORMATION FOR SEQ ID NO:63:   | Joine 200              |
|   | 1007<br>1008<br>1009<br>1010                 | (2) INFORMATION FOR SEQ ID NO:63:   | Joine 200              |
|   | 1007<br>1008<br>1009<br>1010<br>1011         | (2) INFORMATION FOR SEQ ID NO:63:  (i) SEQUENCE CHARACTERISTICS:                            | Joine 200              |
| > | 1007<br>1008<br>1009<br>1010<br>1011<br>1012 | (2) INFORMATION FOR SEQ ID NO:63:  (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 21 base pairs | Joine 200              |
| > | 1007<br>1008<br>1009<br>1010<br>1011         | (2) INFORMATION FOR SEQ ID NO:63:  (i) SEQUENCE CHARACTERISTICS:                            | Joine 200              |

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|   |      |  | INPUT SET: S31624.raw |
|---|------|--|-----------------------|
|   | 1015 | (D) TOPOLOGY: linear                         |                       |
|   | 1016 |  |                       |
|   | 1017 | (ii) MOLECULE TYPE: DNA (genomic)            |                       |
|   | 1018 |  | •                     |
|   | 1019 | (iii) HYPOTHETICAL: NO                       |                       |
|   | 1020 |  |                       |
|   | 1021 | (iv) ANTI-SENSE: NO                          |                       |
|   | 1022 | •  |                       |
|   | 1023 |  |                       |
|   | 1024 |  | 1 4 00.00             |
|   | 1025 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:     | / snell low           |
|   | 1026 |  | /80 07;               |
|   | 1027 | ACTAGTCAGA ATGTGCGGAC G                      | Jonnet enn            |
|   | 1028 | 21   |                       |
|   | 1029 |  |                       |
|   |      |  |                       |
|   | 1030 | (2) INFORMATION FOR SEQ ID NO:64:            |                       |
|   | 1031 |  | ļ · '                 |
|   | 1032 | (i) SEQUENCE CHARACTERISTICS:                |                       |
| > | 1033 | (A) LENGTH: 21 base pairs                    |                       |
|   | 1034 | (B) TYPE: nucleic acid                       |                       |
|   | 1035 | (C) STRANDEDNESS: single                     | 1                     |
|   | 1036 | (D) TOPOLOGY: linear                         |                       |
|   | 1037 |  |                       |
|   | 1038 | <pre>(ii) MOLECULE TYPE: DNA (genomic)</pre> |                       |
|   | 1039 |  |                       |
|   | 1040 | (iii) HYPOTHETICAL: NO                       |                       |
|   | 1041 |  |                       |
|   | 1042 | (iv) ANTI-SENSE: NO                          |                       |
|   | 1043 |  |                       |
|   | 1044 |  |                       |
|   | 1045 |  |                       |
|   | 1046 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:     | 1                     |
|   | 1047 |  | į                     |
|   | 1048 | ACTTATCCTA TTCCGATTCG T                      |                       |
|   | 1049 | 21   |                       |
|   | 1050 |  |                       |
|   | 1051 | (2) INFORMATION FOR SEQ ID NO:65:            |                       |
|   | 1051 | /2/ The origination for Mark to Moroce.      | (   /                 |
|   | 1053 | (i) SEQUENCE CHARACTERISTICS:                |                       |
| > | 1054 | (A) LENGTH: 21 base pairs                    |                       |
| - | 1055 | (B) TYPE: nucleic acid                       | •                     |
|   | 1056 | (C) STRANDEDNESS: single                     |                       |
|   | 1057 | (D) TOPOLOGY: linear                         |                       |
|   | 1058 | (-)  | ,                     |
|   | 1059 | (ii) MOLECULE TYPE: DNA (genomic)            |                       |
|   | 1060 | ,,,  | ,                     |
|   | 1061 | (iii) HYPOTHETICAL: NO                       | •                     |
|   | 1062 | , === /                                      |                       |
|   | 1063 | (iv) ANTI-SENSE: NO                          |                       |
|   | 1064 | , — , ,                                      |                       |
|   | 1065 |  |                       |
|   | 1000 |  |                       |

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INPUT SET: S31624.raw

|   |              |  | INPUT SET: S31624.raw |
|---|--------------|--|-----------------------|
|   | 1066<br>1067 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65: | same end              |
|   | 1068         | (XI) DECORNCE DESCRIPTION. SEQ ID NO.03. | and ever              |
|   | 1069         | ACTTATCCTA TTCCGTTTCG T                  | July 1.               |
|   | 1070         | 21                                       | -                     |
|   | 1071         | <del></del>                              | <b>f</b>              |
|   |              |  |                       |
|   | 1072         | (2) INFORMATION FOR SEQ ID NO:66:        |                       |
|   | 1073         |  | ]                     |
|   | 1074         | (i) SEQUENCE CHARACTERISTICS:            |                       |
| > | 1075         | (A) LENGTH: 21 base pairs                |                       |
|   | 1076         | (B) TYPE: nucleic acid                   | İ                     |
|   | 1077         | (C) STRANDEDNESS: single                 |                       |
|   | 1078         | (D) TOPOLOGY: linear                     |                       |
|   | 1079         | /ii Normourn munn - DWR / non-min        |                       |
|   | 1080         | (ii) MOLECULE TYPE: DNA (genomic)        |                       |
|   | 1081<br>1082 | (iii) HYPOTHETICAL: NO                   |                       |
|   | 1082         | (III) HIPOINDIICAD: NO                   |                       |
|   | 1083         | (iv) ANTI-SENSE: NO                      |                       |
|   | 1085         | (IV) ANII-BENSE. NO                      |                       |
|   | 1086         |  |                       |
|   | 1087         |  |                       |
|   | 1088         | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66: |                       |
|   | 1089         | (,                                       | <u> </u>              |
|   | 1090         | TCTTATCCTC ATGGTCAGAT T                  | }                     |
|   | 1091         | 21                                       |                       |
|   | 1092         |  |                       |
|   | 1093         | (2) INFORMATION FOR SEQ ID NO:67:        |                       |
|   | 1094         | (2) Information for shy in no.07.        | •                     |
|   | 1095         | (i) SEQUENCE CHARACTERISTICS:            |                       |
| > | 1096         | (A) LENGTH: 21 base pairs                |                       |
|   | 1097         | (B) TYPE: nucleic acid                   |                       |
|   | 1098         | (C) STRANDEDNESS: single                 |                       |
|   | 1099         | (D) TOPOLOGY: linear                     |                       |
|   | 1100         | ·  |                       |
|   | 1101         | (ii) MOLECULE TYPE: DNA (genomic)        | j                     |
| • | 1102         |  | 1                     |
|   | 1103         | (iii) HYPOTHETICAL: NO                   | J                     |
|   | 1104         |  |                       |
|   | 1105         | (iv) ANTI-SENSE: NO                      |                       |
|   | 1106         |  | $\Psi$                |
|   | 1107         |  |                       |
|   | 1108         |  |                       |
|   | 1109         | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67: |                       |
|   | 1110         | mmma cmccco. cmcmma a mcc. m             |                       |
|   | 1111         | TTTACTGGGA CTCTTAATCC T                  |                       |
|   | 1112         | 21 .                                     |                       |
|   | 1113         |  |                       |
|   | 1114         | (2) INFORMATION FOR SEQ ID NO:68:        |                       |

1115

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|   |       |   | INPUT SET: S31624.raw |
|---|-------|---|-----------------------|
|   | 1116  | (i) SEQUENCE CHARACTERISTICS:                 |                       |
| > | 1117  | (A) LENGTH: 21 bas pairs                      |                       |
|   | 1118  | (B) TYPE: nucleic acid                        |                       |
|   | 1119  | (C) STRANDEDNESS: single                      |                       |
|   | 1120  | (D) TOPOLOGY: linear                          |                       |
|   | 1121  | , ,   |                       |
|   | 1122  | (ii) MOLECULE TYPE: DNA (genomic)             | 0 /                   |
|   | 1123  | (,, , , , , , , , , , , , ,                   | $\Lambda M \sim$      |
|   | 1124  | (iii) HYPOTHETICAL: NO                        | same                  |
|   | 1125  | (/  |                       |
|   | 1126  | (iv) ANTI-SENSE: NO                           | ſ                     |
|   | 1127  | (17) IMIL BEHOLI NO                           | <b>{</b>              |
|   | 1128  |   |                       |
|   | 1129  |   | •                     |
|   | 1130  | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:      |                       |
|   | 1131  | (AI) DEGORMON DESCRIPTION, DEG 12 MOTOR       |                       |
|   | 1132  | ACTTATCCGG TGCCGCATCG G                       |                       |
|   | 1132  | 21  | •                     |
|   | 1134  | 21  |                       |
|   | 1134  |   |                       |
|   | 1135  | (2) INFORMATION FOR SEQ ID NO:69:             |                       |
|   | 1136  | (2) Intommitton for bly 15 notos.             | *                     |
|   | 1137  | (i) SEQUENCE CHARACTERISTICS:                 |                       |
| > | 1138  | (A) LENGTH: 21 base pairs                     |                       |
|   | 1139  | (B) TYPE: nucleic acid                        |                       |
|   | 1140  | (C) STRANDEDNESS: single                      | •                     |
|   | 1141  | (D) TOPOLOGY: linear                          |                       |
|   | 1142  | (b) Torobosi: linear                          |                       |
|   | 1142  | (ii) MOLECULE TYPE: DNA (genomic)             |                       |
|   | 1143  | (II) MODECOBE IIFE. DNA (genomic)             |                       |
|   | 1144  | (iii) HYPOTHETICAL: NO                        |                       |
|   | 1145  | (III) HIFOHEIICAE. NO                         |                       |
|   | 1146  | (iv) ANTI-SENSE: NO                           |                       |
|   | 1147  | (IV) ANII-SENSE: NO                           |                       |
|   | 1149  |   |                       |
|   | .1150 |   |                       |
|   | 1151  | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:      |                       |
|   | 1151  | • •   |                       |
|   | 1152  | CGGACTCCTT CGCTTCCTAG T                       |                       |
|   | 1154  | 21  |                       |
|   | 1155  | 21  | ·                     |
|   | 1155  |   |                       |
|   | 1156  | (2) INFORMATION FOR SEQ ID NO:70:             |                       |
|   | 1157  | (2) Intomitted tox bug is not to              |                       |
|   | 1158  | (i) SEQUENCE CHARACTERISTICS:                 |                       |
| > | 1159  | (A) LENGTH: 21 base pairs                     | $\mathcal{A}$         |
|   | 1160  | (B) TYPE: nucleic acid                        | •                     |
|   | 1161  | (C) STRANDEDNESS: single                      |                       |
|   | 1161  | (C) STRANDEDNESS: SINGLE (D) TOPOLOGY: linear |                       |
|   | 1162  | (D) TOPOLOGI: Linear                          |                       |
|   | 1163  | (ii) MOLECULE TYPE: DNA (genomic)             |                       |
|   | 1164  | (II) MODECODE TIPE: DNA (Genomic)             |                       |
|   |       | (iii) UVDOTUETTCAL. NO                        |                       |
|   | 1166  | (iii) HYPOTHETICAL: NO                        |                       |

#### RAW SEQUENCE LISTING PATENT APPLICATION US/09/229,751

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INPUT SET: S31624.raw Sign 7/ though 79 mining (brek pages) (iv) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70: TTTAGTGTTC CTCGTATGCC G (2) INFORMATION FOR SEQ ID NO:80: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 1.184 (ii) MOLECULE TYPE: peptide (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80: Asn His Phe Leu Lys Ser Gln Pro Gly Val Val Thr Jege 88 through 98 mining ( hack pager) (2) INFORMATION FOR SEQ ID NO:99: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 11 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99: 

Asn His Phe Leu Pro Lys Val Gly Gly Cys

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|   | 1365 |   |
|---|------|---|
|   | 1387 | (2) INFORMATION FOR SEQ ID NO:101:          |
|   | 1388 |   |
|   | 1389 | (i) SEQUENCE CHARACTERISTICS:               |
| > | 1390 | (A) LENGTH: 21 base pairs                   |
|   | 1391 | (B) TYPE: nucleic acid                      |
|   | 1392 | (C) STRANDEDNESS: single                    |
|   | 1393 | (D) TOPOLOGY: linear                        |
|   | 1394 |   |
|   | 1395 | (ii) MOLECULE TYPE: DNA (genomic)           |
|   | 1396 |   |
|   | 1397 | (iii) HYPOTHETICAL: NO                      |
|   | 1398 | المهمول المعادية                            |
|   | 1399 | (iii) HYPOTHETICAL: NO  (iv) ANTI-SENSE: NO |
|   | 1400 |   |
|   | 1401 |   |
|   | 1402 | <b>~</b>                                    |
|   | 1403 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:   |
|   | 1404 | ,,  |
|   | 1405 | ACGCATCGTT TGCCTTCTCG G                     |
|   | 1406 | 21  |
|   | 1407 |   |
|   | 1408 | (2) INFORMATION FOR SEQ ID NO:102:          |
|   | 1409 |   |
|   | 1410 | (i) SEQUENCE CHARACTERISTICS:               |
| > | 1411 | (A) LENGTH: 21 base pairs                   |
|   | 1412 | (B) TYPE: nucleic acid                      |
|   | 1413 | (C) STRANDEDNESS: single                    |
|   | 1414 | (D) TOPOLOGY: linear                        |
|   | 1415 |   |
|   | 1416 | (ii) MOLECULE TYPE: DNA (genomic)           |
|   | 1417 |   |
|   | 1418 | (iii) HYPOTHETICAL: NO                      |
|   | 1419 |   |
|   | 1420 | (iv) ANTI-SENSE: NO                         |
|   | 1421 |   |
|   | 1422 | . 17  |
|   | 1423 |   |
|   | 1424 | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:   |
|   | 1425 |   |
|   | 1426 | GTTACTAGTA GGGGGAATGT T                     |
|   | 1427 | 21  |
|   | 1428 |   |
|   | 1429 | (2) INFORMATION FOR SEQ ID NO:103:          |
|   | 1430 |   |
|   | 1431 | (i) SEQUENCE CHARACTERISTICS:               |
| > | 1432 | (A) LENGTH: 21 base pairs                   |
|   | 1433 | (B) TYPE: nucleic acid                      |
|   | 1434 | (C) STRANDEDNESS: single                    |
|   | 1435 | (D) TOPOLOGY: linear                        |

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1436
          (ii) MOLECULE TYPE: DNA (genomic)
1437
1438
                                                                frant eval
1439
          (iii) HYPOTHETICAL: NO
1440
          (iv) ANTI-SENSE: NO
1441
1442
1443
1444
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:
1445
1446
      AAGCTGTGGG TGATTCCTCA G
1447
1448
          21
1449
1450
      (2) INFORMATION FOR SEQ ID NO:104:
1451
            (i) SEQUENCE CHARACTERISTICS:
1452
                 (A) LENGTH: 21 base pairs
1453
                 (B) TYPE: nucleic acid
1454
1455
                 (C) STRANDEDNESS: single
                 (D) TOPOLOGY: linear
1456
1457
1458
          (ii) MOLECULE TYPE: DNA (genomic)
1459
          (iii) HYPOTHETICAL: NO
1460
1461
1462
           (iv) ANTI-SENSE: NO
1463
1464
1465
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:
1466
1467
      TATTCGCCTC CTCATAGGCA T
1468
1469
          21
1470
1471
       (2) INFORMATION FOR SEQ ID NO:105:
1472
            (i) SEQUENCE CHARACTERISTICS:
1473
                 (A) LENGTH: 21 base pairs
1474
                 (B) TYPE: nucleic acid
1475
1476
                 (C) STRANDEDNESS: single
1477
                 (D) TOPOLOGY: linear
1478
1479
           (ii) MOLECULE TYPE: DNA (genomic)
1480
1481
          (iii) HYPOTHETICAL: NO
1482
1483
           (iv) ANTI-SENSE: NO
1484
1485
1486
```

#### RAW SEQUENCE LISTING PATENT APPLICATION US/09/229,751

DATE: 04/27/1999 TIME: 10:35:33

INPUT SET: S31624.raw some en (xi) SEQUENCE DESCRIPTION: SEQ ID NO:105: TCGTATCCTC CGTATTTTGA T (2) INFORMATION FOR SEQ ID NO:106: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106: CTTTTGTCGC CTCTGCATCG T (2) INFORMATION FOR SEQ ID NO:107: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: DNA (genomic) (iii) HYPOTHETICAL: NO (iv) ANTI-SENSE: NO (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107: TTTGATTCTC CGCTTCGTCG G (2) INFORMATION FOR SEQ ID NO:108: 

(i) SEQUENCE CHARACTERISTICS:

## RAW SEQUENCE LISTING PATENT APPLICATION US/09/229,751

DATE: 04/27/1999 TIME: 10:35:34

| >               | 1537   | (A) LENGTH: 21 base pairs   |   |
|-----------------|--|---|---|
|                 | 1538   | (B) TYPE: nucleic acid  |   |
|                 | 1539   | (C) STRANDEDNESS: single  |   |
|                 | 1540   | (D) TOPOLOGY: linear  |   |
|                 | 1541   | 1 1 1 1   |   |
|                 | 1542   | (ii) MOLECULE TYPE: DNA (genomic)   |   |
|                 | 1543   |   |   |
|                 | 1544   | (iii) HYPOTHETICAL: NO  |   |
|                 | 1545   |   |   |
|                 | 1546   | (iv) ANTI-SENSE: NO   |   |
|                 | 1547   |   |   |
|                 | 1548   |   |   |
|                 | 1549   |   |   |
|                 | 1550   | (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:   |   |
|                 | 1551   |   |   |
|                 | 1552   | TGGTCGCCGC TGCATAAGCA T   |   |
|                 | 1553   | 21  |   |
|                 | 1554   | leg. 104 messing  |   |
|                 |  | 29-17-17-1  |   |
| >               | 1555   | (2) INFORMATION FOR SEQ ID NO:110:  |   |
| >               | 1555<br>1556   | (2) INFORMATION FOR SEQ ID NO:110:  |   |
| >               |  | (2) INFORMATION FOR SEQ ID NO:110:  (i) SEQUENCE CHARACTERISTICS:  (bed page)   |   |
| >               | 1556   |   | - |
| >               | 1556<br>1557   | (i) SEQUENCE CHARACTERISTICS:   |   |
| >               | 1556<br>1557<br>1558   | (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 7 amino acids  |   |
| >               | 1556<br>1557<br>1558<br>1559   | (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 7 amino acids  (B) TYPE: amino acid  |   |
| >               | 1556<br>1557<br>1558<br>1559<br>1560   | (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 7 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  |   |
| >               | 1556<br>1557<br>1558<br>1559<br>1560<br>1561   | (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 7 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  |   |
| <del>&gt;</del> | 1556<br>1557<br>1558<br>1559<br>1560<br>1561<br>1562   | (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 7 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  |   |
| <del>&gt;</del> | 1556<br>1557<br>1558<br>1559<br>1560<br>1561<br>1562<br>1563   | (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 7 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  |   |
| =><br>d         | 1556<br>1557<br>1558<br>1559<br>1560<br>1561<br>1562<br>1563<br>1564   | (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 7 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: peptide   |   |
| <del></del>     | 1556<br>1557<br>1558<br>1559<br>1560<br>1561<br>1562<br>1563<br>1564<br>1565<br>1566                                 | (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 7 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: peptide   |   |
| <del></del> >   | 1556<br>1557<br>1558<br>1559<br>1560<br>1561<br>1562<br>1563<br>1564<br>1565<br>1566<br>1567                         | (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 7 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: peptide  (iii) HYPOTHETICAL: NO   |   |
| <del></del> >   | 1556<br>1557<br>1558<br>1559<br>1560<br>1561<br>1562<br>1563<br>1564<br>1565<br>1566<br>1567<br>1568<br>1569         | (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 7 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: peptide  (iii) HYPOTHETICAL: NO   |   |
| <del></del> >   | 1556<br>1557<br>1558<br>1559<br>1560<br>1561<br>1562<br>1563<br>1564<br>1565<br>1566<br>1567<br>1568<br>1569<br>1570 | <pre>(i) SEQUENCE CHARACTERISTICS:         (A) LENGTH: 7 amino acids         (B) TYPE: amino acid         (C) STRANDEDNESS: single         (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: peptide  (iii) HYPOTHETICAL: NO  (iv) ANTI-SENSE: NO</pre> |   |
| <del></del> >   | 1556<br>1557<br>1558<br>1559<br>1560<br>1561<br>1562<br>1563<br>1564<br>1565<br>1566<br>1567<br>1568<br>1569         | (i) SEQUENCE CHARACTERISTICS:  (A) LENGTH: 7 amino acids  (B) TYPE: amino acid  (C) STRANDEDNESS: single  (D) TOPOLOGY: linear  (ii) MOLECULE TYPE: peptide  (iii) HYPOTHETICAL: NO   |   |

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Leu Phe Asn Lys His Val Pro Gly Gly Gly Cys

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

Seg 18 merery (sel iten 8 on Eva Jummy Meet)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

Asn His Phe Leu Pro Thr Ala

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

ID NO:31:

99 29,751

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(see I sen 8 on Even

funnary Keet)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Asn Ser Val Thr Leu Glu Pro

) ID NO:45: Segr 46 phoyl 50 mining

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 7 amino acids

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Phe Ser Val Pro Arg Met Pro

Jeg 57 though 59 mining

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

TTTAGTGTTC CTCGTATGCC G 21

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 12 amino acids

D NO:70: Jege 7/ Xhroyd 79 mining

9*9/*72*9,*7\/

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Asn His Phe Leu Met Pro Asn Pro Leu Leu Ala Met

(2) INFORMATION FOR SEQ ID NO:99:

(i) SEQUENCE CHARACTERISTICS:

Segr 88 though 98 mining

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

(2) INFORMATION FOR SEQ ID NO:110:

-- Jeg /09 mining